



#2

OIPE

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/080,839

DATE: 03/08/2002
TIME: 15:17:10

Input Set : A:\TSRI8131.SEQ.TXT
Output Set: N:\CRF3\03082002\J080839.raw

4 <110> APPLICANT: Schimmel, Paul
 5 Wakasugi, Keisuke
 6 Friedlander, Martin
 8 <120> TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
 9 Polypeptides Useful For The Regulation of Angiogenesis
 12 <130> FILE REFERENCE: TSRI-813.1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/080,839
 C--> 14 <141> CURRENT FILING DATE: 2002-02-22
 14 <150> PRIOR APPLICATION NUMBER: 60/270,951
 15 <151> PRIOR FILING DATE: 2001-02-23
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 23 <212> TYPE: PRT
 24 <213> ORGANISM: Artificial Sequence
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: Recombinant human trpRS
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 33 20 25 30
 34 Lys Asp Glu Ile Asp Ser Ala Val Lys Met Leu Val Ser Leu Lys Met
 35 35 40 45
 36 Ser Tyr Lys Ala Ala Ala Gly Glu Asp Tyr Lys Ala Asp Cys Pro Pro
 37 50 55 60
 38 Gly Asn Pro Ala Pro Thr Ser Asn His Gly Pro Asp Ala Thr Glu Ala
 39 65 70 75 80
 40 Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys
 41 85 90 95
 42 Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile
 43 100 105 110
 44 Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
 45 115 120 125
 46 His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn
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 49 145 150 155 160
 50 Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro
 51 165 170 175
 52 Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val
 53 180 185 190

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 56 Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala
 57 210 215 220
 58 Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr
 59 225 230 235 240
 60 Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys
 61 245 250 255
 62 His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser
 63 260 265 270
 64 Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
 65 275 280 285
 66 Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln
 67 290 295 300
 68 Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr
 69 305 310 315 320
 70 Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His
 71 325 330 335
 72 Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala
 73 340 345 350
 74 Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile
 75 355 360 365
 76 Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
 77 370 375 380
 78 Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
 79 385 390 395 400
 80 Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Lys Leu Glu Gln Ile
 81 405 410 415
 82 Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
 83 420 425 430
 84 Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
 85 435 440 445
 86 Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg
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 95 <211> LENGTH: 4877
 96 <212> TYPE: DNA
 97 <213> ORGANISM: Artificial Sequence
 99 <220> FEATURE:
 100 <223> OTHER INFORMATION: Recombinant human mini-TrpRS in pET20B
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112 ttttattta taaggattt tgccgattt ggcctattgg taaaaaatg agctgattt 420
113 acaaaaattt aacgcgaatt ttaacaaaat attaacgtt acaatttcag gtggcactt 480
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115 tccgctcatg agacaataac cctgataaaat gcttcaataa tattgaaaaa ggaagagtt 600
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118 agtgggttac atcgaactgg atctcaacag cgtaagatc ttgagatgtt ttgcggccg 780
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160	cagtaaggca	accccgccag	cctagccgg	tcctcaacga	caggagcacg	atcatgcgca	3300										
161	cccggtggca	ggacccaacg	ctgcccggaga	tctcgatccc	gcgaaattaa	tacgactcac	3360										
162	tatagggaga	ccacaacggt	ttccctctag	aaataatttt	gtttaacttt	aagaaggaga	3420										
163	tatacat	atg	agc	tac	aaa	gct	gcc	gcg	ggg	gag	gat	tac	aag	gct	gac	3469	
164	Met	Ser	Tyr	Lys	Ala	Ala	Gly	Asp	Tyr	Lys	Ala	Asp					
165	1	5	10														
167	tgt	cct	cca	ggg	aac	cca	gca	cct	acc	agt	aat	cat	ggc	cca	gat	gcc	3517
168	Cys	Pro	Pro	Gly	Asn	Pro	Ala	Pro	Thr	Ser	Asn	His	Gly	Pro	Asp	Ala	
169	15	20	25	30													
171	aca	gaa	gct	gaa	gag	gat	ttt	gtg	gac	cca	tgg	aca	gta	cag	aca	agc	3565
172	Thr	Glu	Ala	Glu	Asp	Phe	Val	Asp	Pro	Trp	Thr	Val	Gln	Thr	Ser		
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176	Ser	Ala	Lys	Gly	Ile	Asp	Tyr	Asp	Lys	Leu	Ile	Val	Arg	Phe	Gly	Ser	
177	50	55	60														
179	agt	aaa	att	gac	aaa	gag	cta	ata	aac	cga	ata	gag	aga	gcc	acc	ggc	3661
180	Ser	Lys	Ile	Asp	Lys	Glu	Leu	Ile	Asn	Arg	Ile	Glu	Arg	Ala	Thr	Gly	
181	65	70	75														
183	caa	aga	cca	cac	cac	ttc	ctg	cgc	aga	ggc	atc	ttc	ttc	tca	cac	aga	3709
184	Gln	Arg	Pro	His	His	Phe	Leu	Arg	Arg	Gly	Ile	Phe	Phe	Ser	His	Arg	
185	80	85	90														
187	gat	atg	aat	cag	gtt	ctt	gat	gcc	tat	gaa	aat	aag	cca	ttt	tat		3757
188	Asp	Met	Asn	Gln	Val	Leu	Asp	Ala	Tyr	Glu	Asn	Lys	Lys	Pro	Phe	Tyr	
189	95	100	105	110													
191	ctg	tac	acg	ggc	cgg	ggc	ccc	tct	tct	gaa	gca	atg	cat	gta	ggt	cac	3805
192	Leu	Tyr	Thr	Gly	Arg	Gly	Pro	Ser	Ser	Glu	Ala	Met	His	Val	Gly	His	
193	115	120	125														
195	ctc	att	cca	ttt	att	ttc	aca	aag	tgg	ctc	cag	gat	gta	ttt	aac	gtg	3853
196	Leu	Ile	Pro	Phe	Ile	Phe	Thr	Lys	Trp	Leu	Gln	Asp	Val	Phe	Asn	Val	
197	130	135	140														
199	ccc	ttg	gtc	atc	cag	atg	acg	gat	gac	gag	aag	tat	ctg	tgg	aag	gac	3901
200	Pro	Leu	Val	Ile	Gln	Met	Thr	Asp	Asp	Glu	Lys	Tyr	Leu	Trp	Lys	Asp	
201	145	150	155														
203	ctg	acc	ctg	gac	cag	gcc	tat	ggc	gat	gct	gtt	gag	aat	gcc	aag	gac	3949
204	Leu	Thr	Leu	Asp	Gln	Ala	Tyr	Gly	Asp	Ala	Val	Glu	Asn	Ala	Lys	Asp	
205	160	165	170														
207	atc	atc	gcc	tgt	ggc	ttt	gac	atc	aac	aag	act	ttc	ata	ttc	tct	gac	3997
208	Ile	Ile	Ala	Cys	Gly	Phe	Asp	Ile	Asn	Lys	Thr	Phe	Ile	Phe	Ser	Asp	
209	175	180	185	190													
211	ctg	gac	tac	atg	ggg	atg	agc	tca	ggt	ttc	tac	aaa	aat	gtg	gtg	aag	4045
212	Leu	Asp	Tyr	Met	Gly	Met	Ser	Ser	Gly	Phe	Tyr	Lys	Asn	Val	Val	Lys	
213	195	200	205														
215	att	caa	aag	cat	gtt	acc	ttc	aac	caa	gtg	aaa	ggc	att	ttc	ggc	ttc	4093
216	Ile	Gln	Lys	His	Val	Thr	Phe	Asn	Gln	Val	Lys	Gly	Ile	Phe	Gly	Phe	
217	210	215	220														
219	act	gac	agc	gac	tgc	att	ggg	aag	atc	agt	ttt	cct	gcc	atc	cag	gct	4141
220	Thr	Asp	Ser	Asp	Cys	Ile	Gly	Lys	Ile	Ser	Phe	Pro	Ala	Ile	Gln	Ala	

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225	240	245	250	
227	gat atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt			4237
228	Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe			
229	255	260	265	270
231	aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc			4285
232	Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala			
233	275	280	285	
235	ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa			4333
236	Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys			
237	290	295	300	
239	atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc			4381
240	Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala			
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243	aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga			4429
244	Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg			
245	320	325	330	
247	gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac			4477
248	Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp			
249	335	340	345	350
251	gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac aag ctc			4525
252	Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu			
253	355	360	365	
255	gag cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag			4573
256	Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu			
257	370	375	380	
259	ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac			4621
260	Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His			
261	385	390	395	
263	cag gcc cg ^g aag gag gtc acg gat gag ata gtg aaa gag ttc atg			4669
264	Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met			
265	400	405	410	
267	act ccc cgg aag ctg tcc gac ttt cag aag ctt gcg gcc gca ctc			4717
268	Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu			
269	415	420	425	430
271	gag cac cac cac cac tgagatccgg ctgctaacaa agccccgaaag			4768
272	Glu His His His His His			
273	435			
275	gaagctgagt tggctgctgc caccgctgag caataactag cataaccctt tggggcctct			4828
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279	<211> LENGTH: 437			
280	<212> TYPE: PRT			
281	<213> ORGANISM: Artificial Sequence			
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VERIFICATION SUMMARY

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Input Set : A:\TSRI8131.SEQ.TXT

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date